IN THE SPECIFICATION

After the Abstract on page 44, insert new Sequence Listing pages 1-12 submitted herewith.

Replace the paragraph beginning with "Thus, the present invention relates" on page 3 of the specification with the following paragraph.

> Thus, the present invention relates to a method for the identification of hetero-associating (poly)peptides comprising the steps of:
> (a) providing a library A of (poly)peptides/proteins comprising (poly)peptides A_m having the general formula:
> VAQLXEXVKTLXAXZYELXSXVQRLXEXVAQL (SEQ ID NO. 1)
> wherein X represents a mixture of E, K, Q, and R, and wherein Z represents a mixture of N and V,
> (b) providing a library B of (poly)peptides/proteins comprising (poly)peptides B_n having the general formula:
> VDELXAXVDQLXDXZYALXTXVAQLXKXVEKL (SEQ ID NO. 2)
> wherein X represents a mixture of E, K, Q, and R, and wherein Z represents a mixture of N and V;
> (c) combining in a common medium the (poly)peptides/proteins of said libraries A and B; and
> (d) screening or selecting for a screenable or selectable property caused by the hetero-association of a (poly)peptide A_m with a (poly)peptide B_n.

Replace the paragraph beginning "In another embodiment" on page 5 of the specification with the following paragraph.

> In another embodiment, the present invention relates to a hetero-associating (poly)peptide A_m taken from the list of:
> WINZIPA1: VAQLEEKVKTLRAQNYELKSRVQRLREQVAQL (SEQ ID NO. 3)
> WINZIPA2: VAQLRERVKTLRAQNYELESEVQRLREQVAQL (SEQ ID NO. 4)
> WINZIPA3: VAQLQEKVKTLRARNYELKSEVQRLEEKVAQL (SEQ ID NO. 5)
> WINZIPA4: VAQLEEQVKTLQARNYELKSKVQRLKEKVAQL (SEQ ID NO. 6)
> WINZIPA5: VAQLEERVKTLRAQNYELKSKVQRLEEQVAQL (SEQ ID NO. 7)
> WINZIPA6: VAQLEEQVKTLEAENYELKSKVQRLRERVAQL (SEQ ID NO. 8)
> WINZIPA7: VAQLQEQVKTLEAQNYELESEVQRLKEQVAQL (SEQ ID NO. 9)
> WINZIPA8: VAQLEERVKTLKAENYELESEVQRLKERVAQL (SEQ ID NO. 10)
> WINZIPA9: VAQLEEKVKTLKAKNYELKSKVQRLKEKVAQL (SEQ ID NO. 11)

WINZIPA10: VAQLQEEVKTLQAENYELRSEVQRLEEEVAQL (SEQ ID NO. 12)
WINZIPA11: VAQLRERVKTLRARNYELQSKVQRLKERVAQL (SEQ ID NO. 13)

Replace the paragraph beginning "Furthermore, the present invention" on page 6 of the specification with the following paragraph.

Furthermore, the present invention relates to a hetero-associating (poly)peptide B_n taken from the list of:
WINZIPB1: VDELQAEVDQLQDENYALKTKVAQLRKKVEKL (SEQ ID NO. 14)
WINZIPB2: VDELKAEVDQLQDQNYALRTKVAQLRKEVEKL (SEQ ID NO. 15)
WINZIPB3: VDELEAEVDQLKDQNYALKTKVAQLQKQVEKL (SEQ ID NO. 16)
WINZIPB4: VDELRAKVDQLQDENYALETEVAQLQKRVEKL (SEQ ID NO. 17)
WINZIPB5: VDELEAEVDQLEDQNYALQTRVAQLEKRVEKL (SEQ ID NO. 18)
WINZIPB6: VDELKAKVDQLKDKNYALRTKVAQLRKKVEKL (SEQ ID NO. 19)
WINZIPB7: VDELRAQVDQLQDKNYALRTRVAQLKKRVEKL (SEQ ID NO. 20)
WINZIPB8: VDELQAEVDQLQDQNYALRTQVAQLKKKVEKL (SEQ ID NO. 21)
WINZIPB9: VDELRAQVDQLEDQNYALETQVAQLEKEVEKL (SEQ ID NO. 22)
WINZIPB10: VDELQAKVDQLKDENYALQTKVAQLQKRVEKL (SEQ ID NO. 23)
WINZIPB11: VDELRAEVDQLEDENYALRTRVAQLRKQVEKL (SEQ ID NO. 24)

Replace the paragraph beginning "Trinucleotide codons (27) were used" on page 18 of the specification with the following paragraph.

Trinucleotide codons (27) were used to code for randomized positions, all other positions were made with mononucleotides.
Library A:
TACTGTGGCGCAACTGNNNGAANNNGTGAAAACCCTTNNNGC-
TNNNXXXTATGAACTTNNNTCTNNNGTGAGCGCTTGNNNGAGNNNGT
TGCCCAGCTTGCTA (SEQ ID NO. 25) (encoding
VAQLXEXVKTLXAXZYLXSXV QRLXEXVAQL (SEQ ID NO. 26), wherein X represents a mixture of E, K, Q, and R, and wherein Z represents a mixture of N and V); libraryB:
CTCCGTTGACGAACTGNNNGCTNNNGTTGACCAGCTGNNNGACNNNX
XXTACGCTCTGNNNACCNNNGTTCGCAGCTGNNNAAANNNGTGGAAA

AGCTGTGATA (SEQ ID NO. 27) (encoding VDELXAXVDQLXDXZYALXTXVAQL- XKXVEKL (SEQ ID NO. 28), wherein X represents a mixture of E, K, Q, and R, and wherein Z represents a mixture of N and V) (NNN = equimolar mixture of the trinucleotides AAG, CAG, GAG, CGT; XXX = equimolar mixture of the trinucleotides AAT, GTT).

Replace the paragraph beginning "Generation of the second strand" on page 18 of the specification with the following paragraph.

Generation of the second strand and introduction of SalI and NheI restriction sites were achieved by PCR using the primers prA-fwd: GGAGTACTGGCATGCAGTCGACTACTGTGGCGCAACTG (SEQ ID NO. 29) and prA-rev: GGACTAGTACCTTCGCTAGCAAGCTGGGCAAC (SEQ ID NO. 30) or prB-fwd: GGAGTACTGGCATGCAGTCGACCTCCGTTGACGAACTG (SEQ ID NO. 31) and prB-rev: GGACTAGTGCTAGCTTCTGACAGCTTTTCCAC (SEQ ID NO. 32), respectively. This resulted in a 142 bp double-stranded oligonucleotide for either library.

Replace the paragraph beginning "LibraryA and B were both digested " on page 18 of the specification with the following paragraph.

LibraryA and B were both digested with SalI and NheI, gel purified and ligated to the appropriate vector (Fig 2) yielding the plasmids LibA-DHFR[1], LibB-DHFR[2], LibB-DHFR[2:I114A] (Fig. 2A). After subcloning, the resulting linker between either library and DHFR fragment was: $A(SGTS)_2$ STSSGI (SEQ ID NO. 33) for LibA and $SEA(SGTS)_2STS$ (SEQ ID NO. 34) for LibB. To achieve maximal library representation, the ligation mixes were individually electroporated into XL1-Blue cells and selected with ampicillin on rich medium (LB). A 2- to 7-fold over-representation of each library was obtained. The resulting colonies were pooled and the plasmid DNA purified such that supercoiled plasmid DNA was obtained for cotransformation. The supercoiled DNA was cotransformed in BL21 cells yielding about 4×10^6 double-transformants. We used BL21 cells with a transformation efficiency of no less than 5×10^7 transformants per mg of DNA using 200 pg of DNA, or 2×10^7 transformants per mg using 500 ng of DNA. In cotransformations, the occurrence of double transformation was calculated as the number of colonies growing under selective pressure with trimethoprim (described below) divided by the number growing in the absence, when cotransformed with equal amounts of each